REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated March 9, 2004. In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due reconsideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Status of the Claims

Claims 3-8 are under consideration in this application. Claims 9-13 are being cancelled without prejudice or disclaimer. Claims 3-4 are being amended, as set forth in the above marked-up presentation of the claim amendments, in order to more particularly define and distinctly claim applicants' invention.

Additional Amendments

The claims are being amended to correct formal errors and/or to better recite or describe the features of the present invention as claimed. All the amendments to the claims are supported by the specification. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

Formality Rejection

Claim 3 was rejected under 35 U.S.C. § 112, first paragraph, for containing new matter in lines 8-10 thereof. As indicated, the claims have been amended to replace the *constant* (with factors r and R which are not constants but magnitudes varying for different datasets) as required by the Examiner. Accordingly, the withdrawal of the outstanding informality rejection is in order, and is therefore respectfully solicited.

Previous Prior Art Rejection

Claims 1-2 were previously rejected under 35 U.S.C. 102(b) as being anticipated by an article by Schena et al published on Proceedings of the National Academy of Sciences, Vol. 93, 1996, pp.10614-10619 (hereinafter "Schena"). Applicants hereby distinguish the newly amended claim 3 from Schena.

The method for displaying gene expression data of the invention, as now recited in claim 3, comprises: calculating a first ratio b/a of gene expression levels of a Sample B and a Sample A for each of a plurality of genes in a first experiment; calculating a second ratio c/A of gene expression levels of a Sample C and the Sample A for said each of a plurality of genes in a second experiment; obtaining a mediated (p. 7, line 14) dataset of gene expression levels for the Samples A, B, C expressed as (b/a, c/A, 1) for said each of a plurality of genes; calculating a first magnitude r (p. 16, lines 1-6) of said dataset expressed as $r = \text{sqrt}\{(b/a)^2 + (c/A)^2 + 1\}$; and displaying marks ((1/r)(b/a), (1/r)(c/A), 1/r) of a first product of the first ratio and 1/r, a second product of the second ratio and the 1/r, and the 1/r on coordinate positions with respect to x-, y- and z-axes on a surface of a sphere (Fig. 8; "*Figure 8 is an exemplary display of gene expression data (on a surface of a sphere).*" P. 11, lines 7-8).

As recited in claim 4, the method (Fig. 7) further comprises: calculating a second magnitude R (p. 16, lines 1-7) of said dataset expressed as $R = \text{sqrt}\{(b^2 + c^2 + (a + A)^2)$; and displaying marks ((R/r)(b/a), (R/r)(c/A), R/r) of a third product of the first ratio and R/r, a fourth product of the second ratio and the R/r, and the R/r on coordinate positions with respect to x-, y- and z-axes.

As such, the present invention provides a visual display which is useful in roughly understanding the state of groupings and changes, by comparing expression data of genes from two experiments based on expression data of one sample common to both experiments. In order to compare data of expression levels obtained from different experiments, the expression levels are displayed in three-dimension as linked by the data of the common sample A used in both experiments (Abstract).

In a first experiment, gene expression levels a and b are obtained for Samples A and B. The obtained dataset is (a, b). In a second experiment, gene expression levels A and c are obtained for Sample A and C. The obtained dataset is (A, c). Now, since Sample a is commonly used in the two experiments, the two dataset can be mediated by means of the expression levels for Sample A. The obtained datasets are each rescaled into (1, b/a) and (1, c/A) such that these datasets from different experiments are made comparable with each other. Thus, the mediated dataset (b/a , c/A , 1) is produced, each element representing expression levels of gene for Sample B, C and A. To display this dataset as a 3D graphic, each element (b/a , c/A , 1) is assigned to x-, y-,z-axis of a coordinate.

Different datasets corresponding to different genes are displayed on a 3D graphic. To

make these different datasets comparable with each other, they are rescaled using a factor r. For example, the factor r for the dataset (b/a , c/A , 1) is given as follows:

$r = \text{sqrt}\{ (b/a)^2 + (c/A)^2 + 1\}$.

In other words, the factor r is the length of the vector (b/a, c/A, 1).

Each of the different datasets is rescaled with its own factor r, such as:

$1/ r\ (b/a , c/A , 1) = ((1/ r)(b/a), (1/r)(c/A), (1/ r))$.

Thus, on the screen, the datasets are displayed on a surface of a sphere whose radius is 1, such as shown in Fig. 8. The sphere can be easily expanded or contracted by applying a constant K to all the datasets. For example,

$K/ r\ (b/a , c/A, 1) = ((K/ r)(b/a) , (K/ r)(c/A) , (K/ r))$.

Note, particularly, that the factor r is not a constant and different datasets are given different factor r, whereas K is a constant used for expanding or contracting the sphere but is not an essential element in this method.

In the above, the datasets are rescaled using a factor r, i.e., the magnitude of the datasets are standardized. In order to display the datasets in accordance with their original magnitude, a factor R is further applied. For example, R for the dataset (b/a , c/A , 1) is:

$R = \text{sqrt}\{ (b^2 + c^2 + (a+A)^2\}$.

The factor R is equivalent to the length of the vector (b , c , a+A) and is considered to roughly correspond to the magnitude of the addition of dataset (a , b) and (A , c), because they can be represented as (b , 0 , a) and (0 , c , A) on a x-y-z coordinate for Samples B, C and A. Each of the different datasets is applied its own factor R, such as:

$R/ r\ (b/a , c/A , 1) = ((R/ r)(b/a), (R/ r)(c/A) , (R/ r))$.

Thus, on the screen, each dataset is placed on the coordinate with its own magnitude R, and the datasets are displayed as points within a semitransparent ball whose radius is large enough and constant, such as shown in Fig. 7.

Applicants respectfully contend that Schena fails to teach or suggest such a visual displaying method "using **two ratios** b/a, c/A of gene expression levels of three Samples A, B, C for each of a plurality of genes and 1 **as coordinates with respect to x-, y- and z-axes** to **display marks on a surface of a sphere (* 1/r)** or **in three dimensions (* R/r)** " as does the invention.

In contrast, Schena merely "***takes the average*** *of the ratios of two independent hybridization* (page 10614, 2nd col. last two lines)," and Figs. 2-3 of Schena do not resemble Figs.

7-8 of the invention in any way.

As such, the present invention as now claimed is distinguishable and thereby allowable over the rejection raised in the Office Action. The withdrawal of the outstanding prior art rejections is in order, and is respectfully solicited.

In view of all the above, clear and distinct differences as discussed exist between the present invention as now claimed and the prior art reference upon which the rejections in the Office Action rely, Applicants respectfully contend that the prior art references cannot anticipate the present invention or render the present invention obvious. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicants' undersigned representative at the address and phone number indicated below.

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